w Sequence Listing Error ⬤mmary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/672,725

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 __✓__ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

OIPE

```
     4 <110> APPLICANT: Stocker, Penny J.
     5          Steimel-Crespi, Dorothy T.
     6          Crespi, Charles L.
     7          Rief, Timothy C
     8          Patten, Christopher J.
    10 <120> TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
    13 <130> FILE REFERENCE: G0307/7017
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/672,725
C--> 15 <141> CURRENT FILING DATE: 2000-09-28
    15 <150> PRIOR APPLICATION NUMBER: US 60/156,510
    16 <151> PRIOR FILING DATE: 1999-09-28
    18 <160> NUMBER OF SEQ ID NOS: 32
    20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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ERRORED SEQUENCES

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    23 <211> LENGTH: 4279
    24 <212> TYPE: DNA
    25 <213> ORGANISM: Canis familiaris
    27 <220> FEATURE:
    28 <221> NAME/KEY: CDS
    29 <222> LOCATION: (17)...(3859)
    31 <400> SEQUENCE: 1
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    33                    Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu
    34                     1               5                  10
    36  aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aat gag aag aaa      100
    37  Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Asn Glu Lys Lys
    38          15                  20                  25
    40  gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat      148
    41  Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn
    42      30                  35                  40
    44  tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc      196
    45  Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile
    46   45              50                  55                  60
    48  cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca      244
    49  His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr
    50                  65                  70                  75
    52  gat agc ttt gca aat gca gga att tca aga aac aaa act ttt cca gtt      292
    53  Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val
    54              80                  85                  90
    56  ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat      340
    57  Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His
    58          95                  100                 105
    60  ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt      388
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RAW SEQUENCE LISTING   ·   DATE: 10/06/2000
PATENT APPLICATION: US/09/672,725   TIME: 12:46:04

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

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61   Leu Glu Glu Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly
62       110                     115                 120
64   gct ggc gtg ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg      436
65   Ala Gly Val Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu
66   125                 130                 135                 140
68   gca gca gga aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct      484
69   Ala Ala Gly Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala
70                   145                 150                 155
72   atc atg cga cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag      532
73   Ile Met Arg Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu
74               160                 165                 170
76   ctt aac acc cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att      580
77   Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile
78               175                 180                 185
80   ggc gac aaa att gga atg ttc ttt cac tca ata gca aca ttt ttc acc      628
81   Gly Asp Lys Ile Gly Met Phe Phe His Ser Ile Ala Thr Phe Phe Thr
82       190                 195                 200
84   ggt ttt ata gtg ggg ttt aca cgt ggt tgg aag cta acc ctt gtg att      676
85   Gly Phe Ile Val Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile
86   205                 210                 215                 220
88   ttg gcc atc agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag      724
89   Leu Ala Ile Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys
90                   225                 230                 235
92   ata cta tct tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct      772
93   Ile Leu Ser Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala
94               240                 245                 250
96   gga gca gta gct gaa gaa gtc tta gca gca atc aga act gtg att gcc      820
97   Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala
98               255                 260                 265
100  ttt gga gga caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa      868
101  Phe Gly Gly Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu
102       270                 275                 280
104  gaa gct aaa gga att ggg ata aag aaa gct atc acg gcc aac att tct      916
105  Glu Ala Lys Gly Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser
106  285                 290                 295                 300
108  att ggt gcc gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc      964
109  Ile Gly Ala Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe
110                   305                 310                 315
112  tgg tat ggg acc tcc ttg gtc ctc tcc agt gaa tat tct att gga caa      1012
113  Trp Tyr Gly Thr Ser Leu Val Leu Ser Ser Glu Tyr Ser Ile Gly Gln
114               320                 325                 330
116  gta ctc act gtc ttc ttt tct gta tta att ggg gct ttt agt att gga      1060
117  Val Leu Thr Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly
118               335                 340                 345
120  cag gca tcc cca agc att gaa gca ttt gca aac gca aga gga gca gct      1108
121  Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala
122       350                 355                 360
124  tat gaa atc ttc aag ata att gac aat aaa cca agc att gac agc tat      1156
125  Tyr Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr
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RAW SEQUENCE LISTING   DATE: 10/06/2000
PATENT APPLICATION: US/09/672,725   TIME: 12:46:04

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

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126  365                  370                  375                     380
128  tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc      1204
.129 Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe
130                  385                  390                  395
132  aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta      1252
133  Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu
134                  400                  405                  410
136  aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt      1300
137  Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val
138                  415                  420                  425
140  ggg aac agt ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg      1348
141  Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg
142         430                  435                  440
144  ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att      1396
145  Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile
146  445                  450                  455                  460
148  agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt      1444
149  Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser
150                  465                  470                  475
152  cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat      1492
153  Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr
154                  480                  485                  490
156  ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa      1540
157  Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu
158         495                  500                  505
160  gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act      1588
161  Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr
162         510                  515                  520
164  ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga      1636
165  Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg
166  525                  530                  535                  540
168  atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg      1684
169  Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu
170                  545                  550                  555
172  gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag      1732
173  Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln
174                  560                  565                  570
176  gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct      1780
177  Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala
178         575                  580                  585
180  cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat      1828
181  His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp
182         590                  595                  600
184  gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag      1876
185  Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu
186  605                  610                  615                  620
188  aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa      1924
189  Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu
190                  625                  630                  635
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RAW SEQUENCE LISTING   DATE: 10/06/2000
PATENT APPLICATION: US/09/672,725   TIME: 12:46:04

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

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192   att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc      1972
193   Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala
194                 640                 645                 650
196   ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga      2020
197   Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg
198                 655                 660                 665
200   tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt      2068
201   Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu
202          670                 675                 680
204   ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg      2116
205   Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp
206   685                 690                 695                 700
208   agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt      2164
209   Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly
210                 705                 710                 715
212   ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata      2212
213   Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile
214                 720                 725                 730
216   ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa      2260
217   Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu
218                 735                 740                 745
220   aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt      2308
221   Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu
222          750                 755                 760
224   gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc      2356
225   Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly
226   765                 770                 775                 780
228   aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga      2404
229   Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg
230                 785                 790                 795
232   tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc      2452
233   Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr
234                 800                 805                 810
236   act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa      2500
237   Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys
238                 815                 820                 825
240   ggg gct ata ggt tcc agg ctt gct gtc att acc cag aat ata gca aat      2548
241   Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn
242          830                 835                 840
244   ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca      2596
245   Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr
246   845                 850                 855                 860
248   ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt      2644
249   Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val
250                 865                 870                 875
252   gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta      2692
253   Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu
254                 880                 885                 890
256   gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act      2740
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257  Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr
258          895                     900                 905
260  gtt gtt tct ttg act cgg gag cag aag ttt gaa tac atg tat gca cag     2788
261  Val Val Ser Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln
262          910                     915                 920
264  agt ttg caa gta cca tac aga aac tct ttg agg aaa gca cac atc ttc     2836
265  Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe
266          925                     930                 935                 940
268  ggg gtc tca ttt tct atc acc cag gca atg atg tat ttt tcc tat gct     2884
269  Gly Val Ser Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala
270          945                     950                 955
272  ggc tgt ttc cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac     2932
273  Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn
274          960                     965                 970
276  ttt cag gat gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg     2980
277  Phe Gln Asp Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met
278          975                     980                 985
280  gca gtg ggg cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa     3028
281  Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys
282          990                     995                 1000
284  gta tca gca gcc cac gtc atc atg atc att gaa aaa agc cct ctg att     3076
285  Val Ser Ala Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile
286  1005                    1010                    1015                1020
288  gac agc tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat     3124
289  Asp Ser Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn
290              1025                    1030                    1035
292  gtg aca ttt aat gag gtc gtg ttc aac tat ccc act cga cca gac atc     3172
293  Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile
294              1040                    1045                    1050
296  ccc gtg ctc cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg     3220
297  Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu
298          1055                    1060                    1065
300  gcc ctc gta ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc     3268
301  Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu
302      1070                    1075                    1080
304  cta gag cgc ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc     3316
305  Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly
306  1085                    1090                    1095                1100
308  aaa gag ata aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc     3364
309  Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly
310              1105                    1110                    1115
312  atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac     3412
313  Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn
314              1120                    1125                    1130
316  att gcc tat gga gac aac agc cgg gtc gta tca cat gag gag att atg     3460
317  Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met
318          1135                    1140                    1145
320  cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct     3508
321  Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro
```

```
322     1150              1155              1160
324  gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt      3556
325  Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly
326  1165              1170              1175              1180
328  ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct      3604
329  Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro
330              1185              1190              1195
332  cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt      3652
333  His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
334              1200              1205              1210
336  gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc      3700
337  Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr
338          1215              1220              1225
340  tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta      3748
341  Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu
342      1230              1235              1240
344  ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa      3796
345  Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln
346  1245              1250              1255              1260
348  cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag      3844
349  Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln
350              1265              1270              1275
352  gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tattttttaa    3899
353  Ala Gly Ala Lys Arg
354              1280
356  tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac    3959
357  tatgtagaac tacctgttta acatttcttg ctgcaactga agatcattcc accaagttca    4019
358  gagtcttcag attttataat taaaggaacc aaaagaaaca ttatctgatg gaataaaata    4079
359  ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt    4139
360  gtataatttt tgtttatatt ttatttgtaa cttactgctt tgctgaaaga ttatagaagt    4199
361  ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa acttttatat    4259
362  caaaaaaaaa aaaaaaaaaa                                                4279
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E--> (arrow pointing to line 362)

(handwritten annotation, underline drawn under line 362)

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364  <210> SEQ ID NO: 2
365  <211> LENGTH: 1281
366  <212> TYPE: PRT
367  <213> ORGANISM: Canis familiaris
369  <400> SEQUENCE: 2
370  Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn Phe Trp
371  1               5               10              15
372  Lys Met Gly Lys Lys Ser Lys Lys Asn Glu Lys Lys Glu Lys Lys Pro
373              20              25              30
374  Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn Trp Leu Asp Arg
375          35              40              45
376  Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile His Gly Ala Ala
377  50              55              60
378  Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr Asp Ser Phe Ala
379  65              70              75              80
380  Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val Ile Ile Asn Glu
381              85              90              95
```

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

```
382  Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His Leu Glu Glu Glu
383              100                     105                 110
384  Met Thr Thr Tyr Ala Tyr Tyr Ser Gly Ile Gly Ala Gly Val Leu
385          115                 120                 125
386  Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu Ala Ala Gly Arg
387          130                 135                 140
388  Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala Ile Met Arg Gln
389  145                 150                 155                 160
390  Glu Ile Gly Trp Phe Asp Val His Asp.Val Gly Glu Leu Asn Thr Arg
391                  165                 170                 175
392  Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile Gly Asp Lys Ile
393              180                 185                 190
394  Gly Met Phe Phe His Ser Ile Ala Thr Phe Phe Thr Gly Phe Ile Val
395          195                 200                 205
396  Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile Leu Ala Ile Ser
397          210                 215                 220
398  Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys Ile Leu Ser Ser
399  225                 230                 235                 240
400  Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala Gly Ala Val Ala
401              245                 250                 255
402  Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala Phe Gly Gly Gln
403              260                 265                 270
404  Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu Glu Ala Lys Gly
405          275                 280                 285
406  Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser Ile Gly Ala Ala
407          290                 295                 300
408  Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly Thr
409  305                 310                 315                 320
410  Ser Leu Val Leu Ser Ser Glu Tyr Ser Ile Gly Gln Val Leu Thr Val
411              325                 330                 335
412  Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly Gln Ala Ser Pro
413              340                 345                 350
414  Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala Tyr Glu Ile Phe
415              355                 360                 365
416  Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr Ser Lys Ser Gly
417          370                 375                 380
418  His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe Lys Asn Val His
419  385                 390                 395                 400
420  Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu Lys Gly Leu Asn
421              405                 410                 415
422  Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val Gly Asn Ser Gly
423              420                 425                 430
424  Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg Leu Tyr Asp Pro
425          435                 440                 445
426  Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile Arg Thr Ile Asn
427          450                 455                 460
428  Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser Gln Glu Pro Val
429  465                 470                 475                 480
430  Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr Gly Arg Glu Asn
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431                     485                  490                    495
432    Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu Ala Asn Ala Tyr
433                     500                  505              510
434    Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr Leu Val Gly Glu
435             515                  520                  525
436    Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala
437             530                  535                  540
438    Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala Thr
439    545                  550                  555                  560
440    Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Gln·Val Ala Leu Asp
441                     565                  570              575
442    Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala His Arg Leu Ser
443             580                  585                  590
444    Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp Asp Gly Val Ile
445             595                  600                  605
446    Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu Lys Gly Ile Tyr
447        610                  615                  620
448    Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu Ile Glu Leu Glu
449    625                  630                  635                  640
450    Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala Leu Glu Met Ser
451                     645                  650                  655
452    Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg Ser Thr Arg Arg
453             660                  665                  670
454    Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu Gly Thr Lys Glu
455        675                  680                  685
456    Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp Arg Ile Leu Lys
457        690                  695                  700
458    Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly Ile Phe Cys Ala
459    705                  710                  715                  720
460    Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile Ile Phe Ser Arg
461             725                  730                  735
462    Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu Thr Lys Arg Gln
463             740                  745                  750
464    Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu Gly Ile Ile Ser
465        755                  760                  765
466    Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly Lys Ala Gly Glu
467        770                  775                  780
468    Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg Ser Met Leu Arg
469    785                  790                  795                  800
470    Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr Thr Gly Ala Leu
471                     805                  810              815
472    Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys Gly Ala Ile Gly
473             820                  825                  830
474    Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn Leu Gly Thr Gly
475        835                  840                  845
476    Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr Leu Leu Leu Leu
477        850                  855                  860
478    Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val Glu Met Lys Met
479    865                  870                  875                  880
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    480  Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu Glu Gly Ala Gly
    481           885                     890                     895
    482  Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr Val Val Ser Leu
    483           900                     905                 910
    484  Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln Ser Leu Gln Val
    485       915                     920                 925
    486  Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe Gly Val Ser Phe
    487       930             935                 940
    488  Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala Gly Cys Phe Arg
    489  945             950                 955                 960
    490  Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn Phe Gln Asp Val
    491           965                 970                     975
    492  Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met Ala Val Gly Gln
    493           980                 985                     990
    494  Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys Val Ser Ala Ala
    495       995                 1000                1005
    496  His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile Asp Ser Tyr Ser
    497       1010                1015                1020
    498  Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn Val Thr Phe Asn
E--> 499  1025                1030                1035                104
    500  Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile Pro Val Leu Gln
    501                 1045                1050                1055
    502  Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu Ala Leu Val Gly
    503           1060                1065                1070
    504  Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu Leu Glu Arg Phe
    505           1075                1080                1085
    506  Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly Lys Glu Ile Lys
    507       1090                1095                1100
    508  His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly Ile Val Ser Gln
    509  1105                1110                1115                1120
    510  Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn Ile Ala Tyr Gly
    511           1125                1130                1135
    512  Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met Gln Ala Ala Lys
    513           1140                1145                1150
    514  Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro Glu Lys Tyr Asn
    515       1155                1160                1165
    516  Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly Gly Gln Lys Gln
    517       1170                1175                1180
    518  Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro His Ile Leu Leu
    519  1185                1190                1195                1200
    520  Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Lys Val Val
    521               1205                1210                1215
    522  Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr Cys Ile Val Ile
    523           1220                1225                1230
    524  Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu Ile Val Val Phe
    525       1235                1240                1245
    526  Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln Gln Leu Leu Ala
    527       1250                1255                1260
    528  Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln Ala Gly Ala Lys
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I n v a l i d   a m i n o   a c i d → n u m b e r.

A s n
1 0 4 0

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534  <211> LENGTH: 4317
535  <212> TYPE: DNA
536  <213> ORGANISM: Canis familiaris
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544  gaggtgacg atg gat cct gaa gga ggc cgt aag ggg agt gca gag aag aac     111
545          Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu Lys Asn
546          1               5                       10
548  ttc tgg aaa atg ggc aaa aaa agt aaa aaa gag aag aaa gaa aag aaa      159
549  Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Glu Lys Lys Glu Lys Lys
550   15              20                  25                  30
552  cca act gtc agc acg ttt gca atg ttt cgc tat tca aat tgg ctt gat      207
553  Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn Trp Leu Asp
554              35                  40                  45
556  agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc cat gga gct      255
557  Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile His Gly Ala
558          50                  55                  60
560  gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca gat agc ttt      303
561  Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr Asp Ser Phe
562          65                  70                  75
564  gca aat gca gga att tca aga aac aaa act ttt cca gtt ata att aat      351
565  Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val Ile Ile Asn
566      80                  85                  90
568  gaa agt att acg aac aat aca caa cat ttc atc aac cat ctg gag gag      399
569  Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His Leu Glu Glu
570   95              100                 105                 110
572  gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt gct ggc gtg      447
573  Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly Ala Gly Val
574              115                 120                 125
576  ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg gca gca gga      495
577  Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu Ala Ala Gly
578          130                 135                 140
580  aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct atc atg cga      543
581  Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala Ile Met Arg
582          145                 150                 155
584  cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag ctt aac acc      591
585  Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu Leu Asn Thr
586      160                 165                 170
588  cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att ggc gac aaa      639
589  Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile Gly Asp Lys
590   175             180                 185                 190
592  gtt gga atg ttc ttt caa tca ata gca aca ttt ttc acc ggt ttt ata      687
593  Val Gly Met Phe Phe Gln Ser Ile Ala Thr Phe Phe Thr Gly Phe Ile
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594                    195                200                    205
596  gtg ggg ttt aca cct ggt tgg aag cta acc ctt gtg att ttg gcc atc      735
597  Val Gly Phe Thr Pro Gly Trp Lys Leu Thr Leu Val Ile Leu Ala Ile
598                    210                215                    220
600  agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag ata cta tct      783
601  Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys Ile Leu Ser
602                    225                230                    235
604  tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct gga gca gta      831
605  Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala Gly Ala Val
606              240                245                250
608  gct gaa gaa gtc tta gca gca atc aga act gtg att gcc ttt gga gga      879
609  Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala Phe Gly Gly
610  255                260                265                    270
612  caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa gaa gct aaa      927
613  Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu Glu Ala Lys
614                    275                280                    285
616  aga att ggg ata aag aaa gct atc acg gcc aac att tct att ggt gcc      975
617  Arg Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser Ile Gly Ala
618                    290                295                    300
620  gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc tgg tat ggg      1023
621  Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly
622              305                310                315
624  acc tcc ttg gtc ctc tcc agt gaa tat act att gga cag gta ctc act      1071
625  Thr Ser Leu Val Leu Ser Ser Glu Tyr Thr Ile Gly Gln Val Leu Thr
626        320                325                330
628  gtc ttc ttt tct gta tta att ggg gct ttt agt att gga cag gca tcc      1119
629  Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly Gln Ala Ser
630  335                340                345                    350
632  cca agc att gaa gca ttt gca aac gca aga gga gca gct tat gaa atc      1167
633  Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala Tyr Glu Ile
634              355                360                365
636  ttc aag ata att gac aat aaa cca agc att gac agc tat tcg aag agt      1215
637  Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr Ser Lys Ser
638                    370                375                    380
640  gga cat aaa cca gat aat att aag gga aat ttg gaa ttc aaa aat gtt      1263
641  Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe Lys Asn Val
642              385                390                395
644  cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta aag ggt ctc      1311
645  His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu Lys Gly Leu
646        400                405                410
648  aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt ggg aac agt      1359
649  Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val Gly Asn Ser
650  415                420                425                    430
652  ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg ctc tat gac      1407
653  Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg Leu Tyr Asp
654              435                440                445
656  ccc aca gat ggc atg gtc tgt att gat gga cag gac att agg acc ata      1455
657  Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile Arg Thr Ile
658              450                455                460
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660  aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt cag gag cct   1503
661  Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser Gln Glu Pro
662          465                 470                 475
664  gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat ggc cgc gaa   1551
665  Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr Gly Arg Glu
666          480                 485                 490
668  aat gtc acc atg gat gag att gag aaa gct gtt aag gaa gcc aat gcc   1599
669  Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu Ala Asn Ala
670  495                 500                 505                 510
672  tat gat ttt atc atg aaa cta cct aat aaa ttt gac act ctg gtt gga   1647
673  Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr Leu Val Gly
674          515                 520                 525
676  gag aga ggg gcc cgg ctg agt ggt gga cag aaa cag aga atc gcc att   1695
677  Glu Arg Gly Ala Arg Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile
678          530                 535                 540
680  gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg gat gag gca   1743
681  Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala
682          545                 550                 555
684  acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag gtg gcc ctg   1791
685  Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln Val Ala Leu
686          560                 565                 570
688  gat aag gcc aga aaa ggc cgg act acc att gtg ata gct cat cgt ttg   1839
689  Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala His Arg Leu
690  575                 580                 585                 590
692  tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat gat gga gtc   1887
693  Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp Asp Gly Val
694          595                 600                 605
696  att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag aag ggc att   1935
697  Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu Lys Gly Ile
698          610                 615                 620
700  tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa att gag tta   1983
701  Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu Ile Glu Leu
702          625                 630                 635
704  gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc ttg gaa atg   2031
705  Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala Leu Glu Met
706          640                 645                 650
708  tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga tca act cgc   2079
709  Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg Ser Thr Arg
710  655                 660                 665                 670
712  agg agt ata cat gca cca caa ggc caa gac aga aag ctt ggt aca aaa   2127
713  Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu Gly Thr Lys
714          675                 680                 685
716  gag gac ttg aat gag aat gtt cct tca gtt tcc ttc tgg agg att ctg   2175
717  Glu Asp Leu Asn Glu Asn Val Pro Ser Val Ser Phe Trp Arg Ile Leu
718          690                 695                 700
720  aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt ata ttt tgt   2223
721  Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly Ile Phe Cys
722          705                 710                 715
724  gct att ata aac gga ggc ctg caa cca gca ttt tca ata ata ttt tca   2271
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725  Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile Ile Phe Ser
726      720                 725                 730
728  agg att ata ggg atc ttt acc cga gat gag gat cct gaa aca aaa cga    2319
729  Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu Thr Lys Arg
730  735                 740                 745                 750
732  cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt gga att att    2367
733  Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu Gly Ile Ile
734                      755                 760                 765
736  tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc aaa gct ggg    2415
737  Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly Lys Ala Gly
738                      770                 775                 780
740  gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga tcc atg ctg    2463
741  Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg Ser Met Leu
742          785                 790                 795
744  aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc act gga gca    2511
745  Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr Thr Gly Ala
746      800                 805                 810
748  ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa ggg gct ata    2559
749  Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys Gly Ala Ile
750  815                 820                 825                 830
752  ggt tcc agg ctt gct gtc att acc cag aat ata gca aat ctt ggg aca    2607
753  Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn Leu Gly Thr
754                      835                 840                 845
756  ggc att att ata tcc tta atc tat ggt tgg caa tta aca ctt tta ctc    2655
757  Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr Leu Leu Leu
758                      850                 855                 860
760  tta gca att gta ccc atc att gca ata gca gga gtt gtt gaa atg aaa    2703
761  Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val Glu Met Lys
762          865                 870                 875
764  atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta gaa gga gct    2751
765  Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu Glu Gly Ala
766      880                 885                 890
768  ggg aag att gct aca gaa gcc atc gaa aac ttc cga act gtt gtt tct    2799
769  Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr Val Val Ser
770  895                 900                 905                 910
772  ttg act cgg gag cag aag ttt gaa tac atg tat gca cag agt ttg caa    2847
773  Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln Ser Leu Gln
774                      915                 920                 925
776  gta cca tac aga aac tct ttg agg aaa gca cac atc ttc ggg gtc tca    2895
777  Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe Gly Val Ser
778                      930                 935                 940
780  ttt tct atc acc cag gca atg atg tat ttt tcc tat gct ggc tgt ttc    2943
781  Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala Gly Cys Phe
782          945                 950                 955
784  cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac ttt cag gat    2991
785  Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn Phe Gln Asp
786      960                 965                 970
788  gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg gca gtg ggg    3039
789  Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met Ala Val Gly
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792  cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa gta tca gca      3087
793  Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys Val Ser Ala
794              995              1000             1005
796  gcc cac gtc atc atg atc att gaa aaa agc cct ctg att gac agc tac      3135
797  Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile Asp Ser Tyr
798          1010             1015             1020
800  agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat gtg aca ttt      3183
801  Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn Val Thr Phe
802          1025             1030             1035
804  aat gag gtc gtg ttc aac tat ccc act cga cca gac atc ccc gtg ctc      3231
805  Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile Pro Val Leu
806      1040             1045             1050
808  cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg gcc ctc gta      3279
809  Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu Ala Leu Val
810  1055             1060             1065             1070
812  ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc cta gag cgc      3327
813  Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu Leu Glu Arg
814              1075             1080             1085
816  ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc aaa gag ata      3375
817  Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly Lys Glu Ile
818          1090             1095             1100
820  aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc atc gtg tct      3423
821  Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly Ile Val Ser
822          1105             1110             1115
824  cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac att gcc tat      3471
825  Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn Ile Ala Tyr
826  1120             1125             1130
828  gga gac aac agc cgg gtc gta tca cat gaa gag att atg cag gca gcc      3519
829  Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met Gln Ala Ala
830  1135             1140             1145             1150
832  aag gag gcc aac ata cac cac ttc atc gag aca ctc cct gag aaa tac      3567
833  Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro Glu Lys Tyr
834              1155             1160             1165
836  aac acc aga gta gga gac aaa gga acc cag ctc tct ggt ggc cag aaa      3615
837  Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly Gly Gln Lys
838          1170             1175             1180
840  cag cgc att gcc atá gct cgc gct ctt gtt aga cag cct cat att ttg      3663
841  Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro His Ile Leu
842      1185             1190             1195
844  ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt gaa aag gtt      3711
845  Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Lys Val
846  1200             1205             1210
848  gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc tgc att gtg      3759
849  Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr Cys Ile Val
850  1215             1220             1225             1230
852  atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta ata gtg gtg      3807
853  Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu Ile Val Val
854              1235             1240             1245
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     856  ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa cag ctg ctg        3855
     857  Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln Gln Leu Leu
     858          1250                    1255                    1260
     860  gct cag aaa ggc atc tat ttt tcc atg atc agt gtc cag gct gga gca        3903
     861  Ala Gln Lys Gly Ile Tyr Phe Ser Met Ile Ser Val Gln Ala Gly Ala
     862          1265                    1270                    1275
     864  aag cgc tag tgaactgtgg ccatatgagc tgttaaatat tttttaatat              3952
     865  Lys Arg
     866      1280
     868  ttgtgttaaa acatggcatt taatcaaagt taaaaggtga gcacttactg gaaaaactat     4012
     869  gtagaactac ctgtttaaca tttcttgctg caactgaaga tcattccacc aagttcagag     4072
     870  tcttcagatt ttataattaa aggaaccaaa agaaacatta tctgatggaa taaaatattg     4132
     871  gtgttaattg cattataaaa ttatagagta attcaaagta gattttgtta ataaattgta     4192
     872  taattttgt ttatatttta tttgtaactt actgctttgc tgaaagatta tagaagtggt      4252
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    1652                    Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu
    1653                     1               5                   10
    1655  aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aat gag aag aaa        100
    1656  Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Asn Glu Lys Lys
    1657          15                  20                  25
    1659  gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat       148
    1660  Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn
    1661          30                  35                  40
    1663  tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc       196
    1664  Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile
    1665  45                  50                  55                  60
    1667  cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca       244
    1668  His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr
    1669                  65                  70                  75
    1671  gat agc ttt gca aat gca gga att tca aga aac aaa act ttt cca gtt       292
    1672  Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val
    1673              80                  85                  90
    1675  ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat       340
    1676  Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His
    1677              95                  100                 105
    1679  ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt       388
    1680  Leu Glu Glu Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly
    1681          110                 115                 120
    1683  gct ggc gtg ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg       436
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Invalid end of line numbering. refer to p. 6

4317

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1684  Ala Gly Val Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu
1685  125             130                 135             140
1687  gca gca gga aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct    484
1688  Ala Ala Gly Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala
1689              145                 150                 155
1691  atc atg cga cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag    532
1692  Ile Met Arg Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu
1693              160                 165                 170
1695  ctt aac acc cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att    580
1696  Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile
1697              175                 180                 185
1699  ggc gac aaa att gga atg ttc ttt caa tca ata gca aca ttt ttc acc    628
1700  Gly Asp Lys Ile Gly Met Phe Phe Gln Ser Ile Ala Thr Phe Phe Thr
1701      190                 195                 200
1703  ggt ttt ata gtg ggg ttt aca cgt ggt tgg aag cta acc ctt gtg att    676
1704  Gly Phe Ile Val Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile
1705  205                 210                 215                 220
1707  ttg gcc atc agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag    724
1708  Leu Ala Ile Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys
1709              225                 230                 235
1711  ata cta tct tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct    772
1712  Ile Leu Ser Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala
1713              240                 245                 250
1715  gga gca gta gct gaa gaa gtc tta gca gca atc aga act gtg att gcc    820
1716  Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala
1717          255                 260                 265
1719  ttt gga gga caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa    868
1720  Phe Gly Gly Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu
1721      270                 275                 280
1723  gaa gct aaa gga att ggg ata aag aaa gct atc acg gcc aac att tct    916
1724  Glu Ala Lys Gly Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser
1725  285                 290                 295                 300
1727  att ggt gcc gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc    964
1728  Ile Gly Ala Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe
1729                  305                 310                 315
1731  tgg tat ggg acc tcc ttg gtc ctc tcc agt gaa tat tct att gga caa   1012
1732  Trp Tyr Gly Thr Ser Leu Val Leu Ser Ser Glu Tyr Ser Ile Gly Gln
1733              320                 325                 330
1735  gta ctc act gtc ttc ttt tct gta tta att ggg gct ttt agt att gga   1060
1736  Val Leu Thr Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly
1737              335                 340                 345
1739  cag gca tcc cca agc att gaa gca ttt gca aac gca aga gga gca gct   1108
1740  Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala
1741      350                 355                 360
1743  tat gaa atc ttc aag ata att gac aat aaa cca agc att gac agc tat   1156
1744  Tyr Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr
1745  365                 370                 375                 380
1747  tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc   1204
1748  Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe
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RAW SEQUENCE LISTING   DATE: 10/06/2000
PATENT APPLICATION: US/09/672,725   TIME: 12:46:04

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Output Set: N:\CRF3\10062000\I672725.raw

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1751  aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta      1252
1752  Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu
1753                    400                    405                    410
1755  aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt      1300
1756  Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val
1757                    415                    420                    425
1759  ggg aac agt ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg      1348
1760  Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg
1761       430                    435                    440
1763  ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att      1396
1764  Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile
1765  445                    450                    455                    460
1767  agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt      1444
1768  Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser
1769                    465                    470                    475
1771  cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat      1492
1772  Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr
1773                    480                    485                    490
1775  ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa      1540
1776  Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu
1777            495                    500                    505
1779  gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act      1588
1780  Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr
1781       510                    515                    520
1783  ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga      1636
1784  Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg
1785  525                    530                    535                    540
1787  atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg      1684
1788  Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu
1789                    545                    550                    555
1791  gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag      1732
1792  Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln
1793                    560                    565                    570
1795  gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct      1780
1796  Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala
1797            575                    580                    585
1799  cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat      1828
1800  His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp
1801       590                    595                    600
1803  gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag      1876
1804  Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu
1805  605                    610                    615                    620
1807  aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa      1924
1808  Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu
1809                    625                    630                    635
1811  att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc      1972
1812  Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala
1813            640                    645                    650
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1815  ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga   2020
1816  Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg
1817          655             660             665
1819  tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt   2068
1820  Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu
1821      670             675             680
1823  ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg   2116
1824  Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp
1825  685             690             695             700
1827  agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt   2164
1828  Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly
1829              705             710             715
1831  ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata   2212
1832  Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile
1833          720             725             730
1835  ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa   2260
1836  Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu
1837          735             740             745
1839  aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt   2308
1840  Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu
1841      750             755             760
1843  gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc   2356
1844  Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly
1845  765             770             775             780
1847  aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga   2404
1848  Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg
1849              785             790             795
1851  tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc   2452
1852  Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr
1853          800             805             810
1855  act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa   2500
1856  Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys
1857          815             820             825
1859  ggg gct ata ggt tcc agg ctt gct gtc att acc cag aat ata gca aat   2548
1860  Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn
1861  830             835             840
1863  ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca   2596
1864  Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr
1865  845             850             855             860
1867  ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt   2644
1868  Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val
1869              865             870             875
1871  gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta   2692
1872  Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu
1873              880             885             890
1875  gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act   2740
1876  Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr
1877          895             900             905
1879  gtt gtt tct ttg act cgg gag cag aag ttt gaa tac atg tat gca cag   2788
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1880  Val Val Ser Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln
1881      910                 915                 920
1883  agt ttg caa gta cca tac aga aac tct ttg agg aaa gca cac atc ttc     2836
1884  Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe
1885  925                 930                 935                 940
1887  ggg gtc tca ttt tct atc acc cag gca atg atg tat ttt tcc tat gct     2884
1888  Gly Val Ser Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala
1889                  945                 950                 955
1891  ggc tgt ttc cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac     2932
1892  Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn
1893              960                 965                 970
1895  ttt cag gat gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg     2980
1896  Phe Gln Asp Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met
1897          975                 980                 985
1899  gca gtg ggg cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa     3028
1900  Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys
1901          990                 995                 1000
1903  gta tca gca gcc cac gtc atc atg atc att gaa aaa agc cct ctg att     3076
1904  Val Ser Ala Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile
1905  1005                1010                1015                1020
1907  gac agc tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat     3124
1908  Asp Ser Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn
1909                  1025                1030                1035
1911  gtg aca ttt aat gag gtc gtg ttc aac tat ccc act cga cca gac atc     3172
1912  Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile
1913              1040                1045                1050
1915  ccc gtg ctc cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg     3220
1916  Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu
1917          1055                1060                1065
1919  gcc ctc gta ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc     3268
1920  Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu
1921          1070                1075                1080
1923  cta gag cgc ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc     3316
1924  Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly
1925  1085                1090                1095                1100
1927  aaa gag ata aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc     3364
1928  Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly
1929                  1105                1110                1115
1931  atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac     3412
1932  Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn
1933              1120                1125                1130
1935  att gcc tat gga gac aac agc cgg gtc gta tca cat gag gag att atg     3460
1936  Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met
1937          1135                1140                1145
1939  cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct     3508
1940  Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro
1941  1150                1155                1160
1943  gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt     3556
1944  Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly
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1945 1165                1170                1175                1180
1947 ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct    3604
1948 Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro
1949                1185                1190                1195
1951 cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt    3652
1952 His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
1953                1200                1205                1210
1955 gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc    3700
1956 Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr
1957      1215                1220                1225
1959 tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta    3748
1960 Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu
1961      1230                1235                1240
1963 ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa    3796
1964 Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln
1965 1245                1250                1255                1260
1967 cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag    3844
1968 Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln
1969                1265                1270                1275
1971 gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tattttttaa   3899
1972 Ala Gly Ala Lys Arg
1973                1280
1975 tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac  3959
1976 tatgtagaac tacctgtta acatttcttg ctgcaactga agatcattcc accaagttca    4019
1977 gagtcttcag attttataat taaaggaacc aaaagaaaca ttatctgatg gaataaaata   4079
1978 ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt   4139
1979 gtataatttt tgtttatatt ttatttgtaa cttactgctt tgctgaaaga ttatagaagt   4199
1980 ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa acttttatat   4259
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⌈4279⌉ ~~no end of line numbering. See p. 6~~

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2153 <211> LENGTH: 4279
2154 <212> TYPE: DNA
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2164                     1               5                   10
2166 aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aaa gag aag aaa    100
2167 Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Lys Glu Lys Lys
2168           15              20                  25
2170 gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat    148
2171 Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn
2172      30              35              40
2174 tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc    196
2175 Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile
2176 45              50              55                  60
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2178  cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca      244
2179  His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr
2180                    65                  70                  75
2182  gat agc ttt gca aat gca gga att tca aga aac aaa act ttt cca gtt      292
2183  Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val
2184                80                  85                  90
2186  ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat      340
2187  Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His
2188            95                  100                 105
2190  ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt      388
2191  Leu Glu Glu Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly
2192        110                 115                 120
2194  gct ggc gtg ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg      436
2195  Ala Gly Val Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu
2196  125                 130                 135                 140
2198  gca gca gga aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct      484
2199  Ala Ala Gly Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala
2200                145                 150                 155
2202  atc atg cga cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag      532
2203  Ile Met Arg Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu
2204            160                 165                 170
2206  ctt aac acc cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att      580
2207  Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile
2208            175                 180                 185
2210  ggc gac aaa att gga atg ttc ttt caa tca ata gca aca ttt ttc acc      628
2211  Gly Asp Lys Ile Gly Met Phe Phe Gln Ser Ile Ala Thr Phe Phe Thr
2212        190                 195                 200
2214  ggt ttt ata gtg ggg ttt aca cgt ggt tgg aag cta acc ctt gtg att      676
2215  Gly Phe Ile Val Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile
2216  205                 210                 215                 220
2218  ttg gcc atc agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag      724
2219  Leu Ala Ile Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys
2220                225                 230                 235
2222  ata cta tct tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct      772
2223  Ile Leu Ser Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala
2224            240                 245                 250
2226  gga gca gta gct gaa gaa gtc tta gca gca atc aga act gtg att gcc      820
2227  Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala
2228        255                 260                 265
2230  ttt gga gga caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa      868
2231  Phe Gly Gly Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu
2232        270                 275                 280
2234  gaa gct aaa gga att ggg ata aag aaa gct atc acg gcc aac att tct      916
2235  Glu Ala Lys Gly Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser
2236  285                 290                 295                 300
2238  att ggt gcc gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc      964
2239  Ile Gly Ala Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe
2240                305                 310                 315
2242  tgg tat ggg acc tcc ttg gtc ctc tcc agt gaa tat tct att gga caa     1012
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2243  Trp Tyr Gly Thr Ser Leu Val Leu Ser Ser Glu Tyr Ser Ile Gly Gln
2244          320                     325                 330
2246  gta ctc act gtc ttc ttt tct gta tta att ggg gct ttt agt att gga    1060
2247  Val Leu Thr Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly
2248          335                     340                 345
2250  cag gca tcc cca agc att gaa gca ttt gca aac gca aga gga gca gct    1108
2251  Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala
2252          350                     355                 360
2254  tat gaa atc ttc aag ata att gac aat aaa cca agc att gac agc tat    1156
2255  Tyr Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr
2256  365                     370                     375         380
2258  tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc    1204
2259  Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe
2260               385                     390                 395
2262  aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta    1252
2263  Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu
2264               400                     405                 410
2266  aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt    1300
2267  Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val
2268               415                     420                 425
2270  ggg aac agt ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg    1348
2271  Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg
2272          430                     435                 440
2274  ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att    1396
2275  Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile
2276  445                     450                     455         460
2278  agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt    1444
2279  Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser
2280               465                     470                 475
2282  cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat    1492
2283  Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr
2284               480                     485                 490
2286  ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa    1540
2287  Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu
2288               495                     500                 505
2290  gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act    1588
2291  Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr
2292          510                     515                 520
2294  ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga    1636
2295  Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg
2296  525                     530                     535         540
2298  atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg    1684
2299  Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu
2300               545                     550                 555
2302  gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag    1732
2303  Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln
2304               560                     565                 570
2306  gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct    1780
2307  Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala
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2308          575                580                585
2310  cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat    1828
2311  His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp
2312       590                595                600
2314  gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag    1876
2315  Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu
2316  605                610                615                620
2318  aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa    1924
2319  Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu
2320                625                630                635
2322  att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc    1972
2323  Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala
2324            640                645                650
2326  ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga    2020
2327  Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg
2328            655                660                665
2330  tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt    2068
2331  Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu
2332       670                675                680
2334  ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg    2116
2335  Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp
2336  685                690                695                700
2338  agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt    2164
2339  Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly
2340                705                710                715
2342  ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata    2212
2343  Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile
2344            720                725                730
2346  ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa    2260
2347  Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu
2348            735                740                745
2350  aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt    2308
2351  Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu
2352       750                755                760
2354  gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc    2356
2355  Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly
2356  765                770                775                780
2358  aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga    2404
2359  Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg
2360                785                790                795
2362  tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc    2452
2363  Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr
2364            800                805                810
2366  act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa    2500
2367  Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys
2368            815                820                825
2370  ggg gct ata ggt tcc agg ctt gct gtc att acc cag aat ata gca aat    2548
2371  Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn
2372       830                835                840
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2374  ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca    2596
2375  Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr
2376  845                     850                 855                 860
2378  ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt    2644
2379  Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val
2380                      865                 870                 875
2382  gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta    2692
2383  Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu
2384                  880                 885                 890
2386  gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act    2740
2387  Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr
2388              895                 900                 905
2390  gtt gtt tct ttg act cgg gag cag aag ttt gaa tac atg tat gca cag    2788
2391  Val Val Ser Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln
2392          910                 915                 920
2394  agt ttg caa gta cca tac aga aac tct ttg agg aaa gca cac atc ttc    2836
2395  Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe
2396  925                 930                 935                 940
2398  ggg gtc tca ttt tct atc acc cag gca atg atg tat ttt tcc tat gct    2884
2399  Gly Val Ser Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala
2400                  945                 950                 955
2402  ggc tgt ttc cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac    2932
2403  Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn
2404              960                 965                 970
2406  ttt cag gat gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg    2980
2407  Phe Gln Asp Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met
2408              975                 980                 985
2410  gca gtg ggg cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa    3028
2411  Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys
2412          990                 995                 1000
2414  gta tca gca gcc cac gtc atc atg atc att gaa aaa agc cct ctg att    3076
2415  Val Ser Ala Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile
2416  1005                1010                1015                1020
2418  gac agc tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat    3124
2419  Asp Ser Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn
2420                  1025                1030                1035
2422  gtg aca ttt aat gag gtc gtg ttc aac tat ccc act cga cca gac atc    3172
2423  Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile
2424              1040                1045                1050
2426  ccc gtg ctc cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg    3220
2427  Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu
2428          1055                1060                1065
2430  gcc ctc gta ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc    3268
2431  Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu
2432      1070                1075                1080
2434  cta gag cgc ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc    3316
2435  Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly
2436  1085                1090                1095                1100
2438  aaa gag ata aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc    3364
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                RAW SEQUENCE LISTING              DATE: 10/06/2000
                PATENT APPLICATION:  US/09/672,725  TIME: 12:46:04

                Input Set : A:\485402_1.txt
                Output Set: N:\CRF3\10062000\I672725.raw

2439  Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly
2440              1105                1110                1115
2442  atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac   3412
2443  Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn
2444              1120                1125                1130
2446  att gcc tat gga gac aac agc cgg gtc gta tca cat gaa gag att atg   3460
2447  Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met
2448              1135                1140                1145
2450  cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct   3508
2451  Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro
2452              1150                1155                1160
2454  gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt   3556
2455  Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly
2456  1165                1170                1175                1180
2458  ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct   3604
2459  Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro
2460              1185                1190                1195
2462  cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt   3652
2463  His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
2464              1200                1205                1210
2466  gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc   3700
2467  Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr
2468              1215                1220                1225
2470  tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta   3748
2471  Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu
2472      1230                1235                1240
2474  ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa   3796
2475  Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln
2476  1245                1250                1255                1260
2478  cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag   3844
2479  Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln
2480              1265                1270                1275
2482  gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tattttttaa   3899
2483  Ala Gly Ala Lys Arg
2484              1280
2486  tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac   3959
2487  tatgtagaac tacctgttta acatttcttg ctgcaactga agatcattcc accaagttca   4019
2488  gagtcttcag attttatataat taaaggaacc aaaagaaaca ttatctgatg gaataaaata   4079
2489  ctggtgttaa ttgcattata aaattataga gtaattcaaa gtagattttg ttaataaatt   4139
2490  gtataatttt tgtttatatt ttatttgtaa cttactgctt tgctgaaaga ttatagaagt   4199
2491  ggtaaaaagt actgaatgtt tgaataaagt gctagctata ataaaactaa acttttatat   4259
E--> 2492  caaaaaaaaa aaaaaaaaaa                                            4279
2663  <210> SEQ ID NO: 26
2664  <211> LENGTH: 4279
2665  <212> TYPE: DNA
2666  <213> ORGANISM: Canis familiaris
2668  <220> FEATURE:
2669  <221> NAME/KEY: CDS
2670  <222> LOCATION: (17)...(3859)
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(4279) refer to p.6

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2672 <400> SEQUENCE: 26
2673 ggagcgcgag gtcggg atg gat cct gaa gga ggc cgt aag ggg agt gca gag        52
2674                    Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu
2675                     1               5                  10
2677 aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aaa gag aag aaa         100
2678 Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Lys Glu Lys Lys
2679             15                  20                  25
2681 gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat        148
2682 Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn
2683         30                  35                  40
2685 tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc        196
2686 Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile
2687 45                  50                  55                  60
2689 cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca        244
2690 His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr
2691                     65                  70                  75
2693 gat agc ttt gca aat gca gga att tca aga aac aaa act ttt cca gtt        292
2694 Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val
2695                 80                  85                  90
2697 ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat        340
2698 Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His
2699             95                  100                 105
2701 ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt        388
2702 Leu Glu Glu Glu Met Thr Thr Tyr Ala Tyr Tyr Tyr Ser Gly Ile Gly
2703         110                 115                 120
2705 gct ggc gtg ctg gtg gct gct tac atc cag gtt tca ttc tgg tgc ctg        436
2706 Ala Gly Val Leu Val Ala Ala Tyr Ile Gln Val Ser Phe Trp Cys Leu
2707 125                 130                 135                 140
2709 gca gca gga aga cag ata ctc aaa att aga aaa caa ttt ttt cat gct        484
2710 Ala Ala Gly Arg Gln Ile Leu Lys Ile Arg Lys Gln Phe Phe His Ala
2711                     145                 150                 155
2713 atc atg cga cag gag att ggc tgg ttt gac gtg cat gac gtt ggg gag        532
2714 Ile Met Arg Gln Glu Ile Gly Trp Phe Asp Val His Asp Val Gly Glu
2715                 160                 165                 170
2717 ctt aac acc cgg ctc aca gac gat gtc tcc aaa atc aat gaa gga att       580
2718 Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys Ile Asn Glu Gly Ile
2719             175                 180                 185
2721 ggc gac aaa att gga atg ttc ttt caa tca ata gca aca ttt ttc acc       628
2722 Gly Asp Lys Ile Gly Met Phe Phe Gln Ser Ile Ala Thr Phe Phe Thr
2723         190                 195                 200
2725 ggt ttt ata gtg ggg ttt aca cgt ggt tgg aag cta acc ctt gtg att      676
2726 Gly Phe Ile Val Gly Phe Thr Arg Gly Trp Lys Leu Thr Leu Val Ile
2727 205                 210                 215                 220
2729 .ttg gcc atc agc cct gtt ctt gga ctt tca gcc gcc atc tgg gca aag     724
2730 Leu Ala Ile Ser Pro Val Leu Gly Leu Ser Ala Ala Ile Trp Ala Lys
2731                     225                 230                 235
2733 ata cta tct tca ttt act gat aaa gaa ctc ttg gcc tat gca aaa gct      772
2734 Ile Leu Ser Ser Phe Thr Asp Lys Glu Leu Leu Ala Tyr Ala Lys Ala
2735                 240                 245                 250
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2737  gga gca gta gct gaa gaa gtc tta gca gca atc aga act gtg att gcc      820
2738  Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile Arg Thr Val Ile Ala
2739          255                     260                     265
2741  ttt gga gga caa aag aaa gaa ctt gaa agg tac aac aaa aat tta gaa      868
2742  Phe Gly Gly Gln Lys Lys Glu Leu Glu Arg Tyr Asn Lys Asn Leu Glu
2743          270                     275                     280
2745  gaa gct aaa gga att ggg ata aag aaa gct atc acg gcc aac att tct      916
2746  Glu Ala Lys Gly Ile Gly Ile Lys Lys Ala Ile Thr Ala Asn Ile Ser
2747  285                     290                     295                 300
2749  att ggt gcc gct ttc tta ttg atc tat gca tca tat gct ctg gct ttc      964
2750  Ile Gly Ala Ala Phe Leu Leu Ile Tyr Ala Ser Tyr Ala Leu Ala Phe
2751                          305                     310                 315
2753  tgg tat ggg acc tcc ttg gtc ctc tcc agt gaa tat act att gga caa     1012
2754  Trp Tyr Gly Thr Ser Leu Val Leu Ser Ser Glu Tyr Thr Ile Gly Gln
2755                  320                     325                     330
2757  gta ctc act gtc ttc ttt tct gta tta att ggg gct ttt agt att gga     1060
2758  Val Leu Thr Val Phe Phe Ser Val Leu Ile Gly Ala Phe Ser Ile Gly
2759              335                     340                     345
2761  cag gca tcc cca agc att gaa gca ttt gca aac gca aga gga gca gct     1108
2762  Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn Ala Arg Gly Ala Ala
2763          350                     355                     360
2765  tat gaa atc ttc aag ata att gac aat aaa cca agc att gac agc tat     1156
2766  Tyr Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro Ser Ile Asp Ser Tyr
2767  365                     370                     375                 380
2769  tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc     1204
2770  Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe
2771                  385                     390                     395
2773  aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta     1252
2774  Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu
2775                  400                     405                     410
2777  aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt     1300
2778  Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val
2779              415                     420                     425
2781  ggg aac agt ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg     1348
2782  Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg
2783          430                     435                     440
2785  ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att     1396
2786  Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile
2787  445                     450                     455                 460
2789  agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt     1444
2790  Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser
2791                  465                     470                     475
2793  cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat     1492
2794  Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr
2795              480                     485                     490
2797  ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa     1540
2798  Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu
2799          495                     500                     505
2801  gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act     1588
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2802  Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr
2803          510                 515                 520
2805  ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga    1636
2806  Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg
2807  525                 530                 535                 540
2809  atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg    1684
2810  Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu
2811                      545                 550                 555
2813  gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag    1732
2814  Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln
2815                  560                 565                 570
2817  gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct    1780
2818  Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala
2819              575                 580                 585
2821  cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat    1828
2822  His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp
2823          590                 595                 600
2825  gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag    1876
2826  Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu
2827  605                 610                 615                 620
2829  aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa    1924
2830  Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu
2831                      625                 630                 635
2833  att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc    1972
2834  Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala
2835              640                 645                 650
2837  ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga    2020
2838  Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg
2839          655                 660                 665
2841  tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt    2068
2842  Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu
2843          670                 675                 680
2845  ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg    2116
2846  Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp
2847  685                 690                 695                 700
2849  agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt    2164
2850  Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly
2851                      705                 710                 715
2853  ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata    2212
2854  Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile
2855                      720                 725                 730
2857  ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa    2260
2858  Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu
2859          735                 740                 745
2861  aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt    2308
2862  Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu
2863          750                 755                 760
2865  gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc    2356
2866  Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly
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2867 765                   770                   775                   780
2869 aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga      2404
2870 Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg
2871                   785                   790                   795
2873 tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc      2452
2874 Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr
2875                   800                   805                   810
2877 act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa      2500
2878 Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys
2879         815                   820                   825
2881 ggg gct ata ggt tcc agg ctt gct gtc att acc cag aat ata gca aat      2548
2882 Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn
2883         830                   835                   840
2885 ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca      2596
2886 Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr
2887 845                   850                   855                   860
2889 ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt      2644
2890 Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val
2891                   865                   870                   875
2893 gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta      2692
2894 Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu
2895                   880                   885                   890
2897 gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act      2740
2898 Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr
2899         895                   900                   905
2901 gtt gtt tct ttg act cgg gag cag aag ttt gaa tac atg tat gca cag      2788
2902 Val Val Ser Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln
2903         910                   915                   920
2905 agt ttg caa gta cca tac aga aac tct ttg agg aaa gca cac atc ttc      2836
2906 Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe
2907 925                   930                   935                   940
2909 ggg gtc tca ttt tct atc acc cag gca atg atg tat ttt tcc tat gct      2884
2910 Gly Val Ser Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala
2911                   945                   950                   955
2913 ggc tgt ttc cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac      2932
2914 Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn
2915                   960                   965                   970
2917 ttt cag gat gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg      2980
2918 Phe Gln Asp Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met
2919                   975                   980                   985
2921 gca gtg ggg cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa      3028
2922 Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys
2923         990                   995                   1000
2925 gta tca gca gcc cac gtc atc atg atc att gaa aaa agc cct ctg att      3076
2926 Val Ser Ala Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile
2927 1005                  1010                  1015                  1020
2929 gac agc tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat      3124
2930 Asp Ser Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn
2931                   1025                  1030                  1035
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2933  gtg aca ttt aat gag gtc gtg ttc aac tat ccc act cga cca gac atc      3172
2934  Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile
2935      1040               1045               1050
2937  ccc gtg ctc cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg      3220
2938  Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu
2939      1055               1060               1065
2941  gcc ctc gta ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc      3268
2942  Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu
2943      1070               1075               1080
2945  cta gag cgc ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc      3316
2946  Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly
2947  1085               1090               1095               1100
2949  aaa gag ata aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc      3364
2950  Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly
2951               1105               1110               1115
2953  atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac      3412
2954  Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn
2955               1120               1125               1130
2957  att gcc tat gga gac aac agc cgg gtc gta tca cat gaa gag att gtg      3460
2958  Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Val
2959               1135               1140               1145
2961  cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct      3508
2962  Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro
2963      1150               1155               1160
2965  gag aaa tac aac acc aga gta gga gac aaa gga acc cag ctc tct ggt      3556
2966  Glu Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln Leu Ser Gly
2967  1165               1170               1175               1180
2969  ggc cag aaa cag cgc att gcc ata gct cgc gct ctt gtt aga cag cct      3604
2970  Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Gln Pro
2971               1185               1190               1195
2973  cat att ttg ctt ttg gat gaa gct aca tca gct ctg gat aca gaa agt      3652
2974  His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
2975               1200               1205               1210
2977  gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc aga gaa ggc cgc acc      3700
2978  Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr
2979               1215               1220               1225
2981  tgc att gtg atc gcc cac cgc ttg tcc acc atc cag aat gca gat tta      3748
2982  Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu
2983      1230               1235               1240
2985  ata gtg gtg ttt cag aat ggc aaa gtc aag gag cat ggc aca cat caa      3796
2986  Ile Val Val Phe Gln Asn Gly Lys Val Lys Glu His Gly Thr His Gln
2987  1245               1250               1255               1260
2989  cag ctg ctg gcc cag aaa ggc atc tat ttt tcc atg gtc agt gtc cag      3844
2990  Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val Ser Val Gln
2991               1265               1270               1275
2993  gct gga gca aag cgc tagtgaactg tggccatatg agctgttaaa tatttttaa      3899
2994  Ala Gly Ala Lys Arg
2995               1280
2997  tatttgtgtt aaaacatggc atttaatcaa agttaaaagg tgagcactta ctggaaaaac  3959
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   2998  tatgtagaac  tacctgttta  acatttcttg  ctgcaactga  agatcattcc  accaagttca  4019
   2999  gagtcttcag  attttataat  taaaggaacc  aaaagaaaca  ttatctgatg  gaataaaata  4079
   3000  ctggtgttaa  ttgcattata  aaattataga  gtaattcaaa  gtagattttg  ttaataaatt  4139
   3001  gtataatttt  tgtttatatt  ttatttgtaa  cttactgctt  tgctgaaaga  ttatagaagt  4199
   3002  ggtaaaaagt  actgaatgtt  tgaataaagt  gctagctata  ataaaactaa  acttttatat  4259
E--> 3003  caaaaaaaaa  aaaaaaaaaa                                                  4279
```

(4279) refer to p.6

<210> 28   Seq #28
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 28
nnttttttttt tttttttttt tttttttttt ttcgccggcg acttaagatc tt   52

missing mandatory <220> to <223> features to explain "n's" in sequence. See #10 on Error Summary Sheet.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/672,725   DATE: 10/06/2000
                                       TIME: 12:46:06

Input Set : A:\485402_1.txt
Output Set: N:\CRF3\10062000\I672725.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:362 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:362 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:1
L:499 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:874 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:4317 SEQ:3
L:1981 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:1981 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:22
L:2492 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:2492 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:24
L:3003 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:3003 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4279 Found:4259 SEQ:26
L:3183 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:3183 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:3183 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28